

What is claimed is:

1. Method for the identification of genes and genetic signals based on the structural properties of DNA double-helix comprising the following steps:

A - using the classical physical model of helix-coil transitions,

B - calculating stability curves (probabilities of opening of the DNA double-helix, along a given sequence) by algorithmic methods,

C - determining the disruption in the linear DNA for different temperatures,

D - analysing the stability curves for the detection of genetic signals (disruption of the double-helix) or the identification of coding regions (simple genes or exons in split genes, regions of high thermal stability), and optionally,

E - based on the structural informations, performing classical sequence analysis (donor/acceptor sites, start and codon stops, in correspondence with the frontiers identified in the stability curves and open reading frames analyses) for completing the identification of genes.

2. Method according to claim 1 , characterized by an identification and ab initio prediction method of coding regions comprising simple genes (without introns) and/or exons in split genes (containing exons) in various genomes.

3. Method according to claim 1 and claim 2 characterized by a procedure for the annotation of the various genomes comprising simple genes (without introns) and/or exons in split genes (containing introns) in various genomes characterized by performing the steps A to E of claim 1.

4. Method according to claim 1 characterized by an ab initio prediction method for the identification of genetic signals in various genomes comprising promoters or regulatory sequences characterized by the propensity of opening the DNA double helix [easily melt-region]
5. Use of the method as claimed in claims 1 to 4 for the identification of genes and genetic signals in various genomes
6. Use of the method according to claim 5 wherein the genome is an eukaryotic genome.